

0399

0500/0280
OPIE

#2

P5

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/024,632

DATE: 01/15/2002

TIME: 17:46:56

Input Set : N:\paola\10024632.txt

Output Set: N:\CRF3\01152002\J024632.raw

3 <110> APPLICANT: Monsanto Technology LLC
 4 He, Steve S.
 5 Dotson, Stanton B.
 7 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL
 PROLIFERATION AND
 8 GROWTH AND USES THEREOF
 10 <130> FILE REFERENCE: 38-21(51837)B
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/024,632
 C--> 12 <141> CURRENT FILING DATE: 2001-12-19
 12 <150> PRIOR APPLICATION NUMBER: US 60/257,896
 13 <151> PRIOR FILING DATE: 2000-12-21
 15 <160> NUMBER OF SEQ ID NOS: 33
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2344
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Glycine max
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (242)..(2233)
 27 <223> OTHER INFORMATION:
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 35 gcagagatta acatgatgat tagtttattt gccaggaat gccttccttc gtgagatata 180
 37 aactgtctagc aatttcaaat cttttcgagt aaccaaaaag aaaaaaacaa aaagcaagaa 240
 39 g atg aag cgc ata aat gag agt aac aac acc gat gat gga aac aat cat 289
 40 Met Lys Arg Ile Asn Glu Ser Asn Asn Thr Asp Asp Gly Asn Asn His
 41 1 5 10 15
 43 aac tgg ttg ggg ttc tct ctc tca ccc cac atg aaa atg gag gct act 337
 44 Asn Trp Leu Gly Phe Ser Leu Ser Pro His Met Lys Met Gly Ala Thr
 45 20 25 30
 47 tca gca gcc act gtt ccg aca acc ttc tac atg tcc cct tct caa tct 385
 48 Ser Ala Ala Thr Val Pro Thr Thr Phe Tyr Met Ser Pro Ser Gln Ser
 49 35 40 45
 51 cac ttg tcc aac ttc gga atg tgt tac ggt gtc gga gaa aat ggt aac 433
 52 His Leu Ser Asn Phe Gly Met Cys Tyr Gly Val Gly Glu Asn Gly Asn
 53 50 55 60
 55 ttc cat tct cca ctt acg gtt atg cct ctc aag tct gat ggg tca ctt 481
 56 Phe His Ser Pro Leu Thr Val Met Pro Leu Lys Ser Asp Gly Ser Leu
 57 65 70 75 80
 59 tgt atc ttg gaa gct ctc aaa aga tca caa acg caa gtg atg gtg cca 529
 60 Cys Ile Leu Glu Ala Leu Lys Arg Ser Gln Thr Gln Val Met Val Pro
 61 85 90 95
 63 act tcg tct ccg aaa ttg gag gac ttt cta ggt ggt gca act atg gga 577
 64 Thr Ser Ser Pro Lys Leu Glu Asp Phe Leu Gly Gly Ala Thr Met Gly
 65 100 105 110
 67 act cac gaa tat gga agc cac gag aga ggt ttg agc cta gac agc atc 625

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72	Tyr	Tyr	Asn	Ser	Gln	Asn	Ala	Glu	Ala	Gln	Pro	Asn	Arg	Asp	Leu	Leu	
73			130				135					140					
75	tca	caa	ccc	ttc	agg	caa	caa	ggt	cat	atg	agt	gtc	caa	aca	cac	cct	721
76	Ser	Gln	Pro	Phe	Arg	Gln	Gln	Gly	His	Met	Ser	Val	Gln	Thr	His	Pro	
77	145					150					155					160	
79	tat	tac	tca	ggc	ctt	gct	tgc	cat	ggt	tta	tat	caa	gca	ccg	ttg	gag	769
80	Tyr	Tyr	Ser	Gly	Leu	Ala	Cys	His	Gly	Leu	Tyr	Gln	Ala	Pro	Leu	Glu	
81					165					170					175		
83	gaa	gaa	aca	aca	aag	gaa	acg	cac	gtg	tgc	gat	tgc	agc	tcc	cta	atg	817
84	Glu	Glu	Thr	Thr	Lys	Glu	Thr	His	Val	Ser	Asp	Cys	Ser	Ser	Ser	Leu	Met
85					180				185				190				
87	cct	caa	atg	aca	gaa	ggc	ttg	aaa	aac	tgg	gtg	gct	cca	aca	agg	gag	865
88	Pro	Gln	Met	Thr	Glu	Gly	Leu	Lys	Asn	Trp	Val	Ala	Pro	Thr	Arg	Glu	
89			195					200				205					
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92	Phe	Ser	Thr	His	Gln	Val	Leu	Glu	Gln	Met	Asn	Cys	Gly	Met			
93			210				215					220					
95	ggg	aat	gag	aga	aat	ggt	gtg	tct	tta	gga	tct	gtg	ggg	tgt	gga	gag	961
96	Gly	Asn	Glu	Arg	Asn	Gly	Val	Ser	Leu	Gly	Ser	Val	Gly	Cys	Gly	Glu	
97	225				230					235					240		
99	tta	cag	tct	cta	agc	tta	tct	atg	agt	cct	ggt	tct	cag	tct	agt	tgt	1009
100	Leu	Gln	Ser	Leu	Ser	Leu	Ser	Met	Ser	Pro	Gly	Ser	Gln	Ser	Ser	Cys	
101					245					250					255		
103	gtc	act	gct	cct	tct	gga	aca	gat	tct	gtt	gct	gtg	gat	gca	aag	aag	1057
104	Val	Thr	Ala	Pro	Ser	Gly	Thr	Asp	Ser	Val	Ala	Val	Asp	Ala	Lys	Lys	
105					260				265				270				
107	aga	ggg	cat	gct	aaa	ctt	ggt	cag	aag	cag	cct	gtg	cat	aga	aaa	tct	1105
108	Arg	Gly	His	Ala	Lys	Leu	Gly	Gln	Lys	Gln	Pro	Val	His	Arg	Lys	Ser	
109					275				280				285				
111	atc	gac	aca	ttt	ggg	caa	aga	acc	tgc	cag	tat	aga	ggt	gtc	aca	agg	1153
112	Ile	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Gln	Tyr	Arg	Gly	Val	Thr	Arg	
113					290			295				300					
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116	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp	Leu	Asn	Ser	Cys	
117	305				310					315					320		
119	aag	aag	gaa	ggg	caa	act	agg	aaa	gga	cga	caa	gtg	tat	ttg	ggg	ggt	1249
120	Lys	Lys	Glu	Gly	Gln	Thr	Arg	Lys	Gly	Arg	Gln	Val	Tyr	Leu	Gly	Gly	
121					325					330					335		
123	tat	gat	atg	gag	gag	aaa	gct	gca	aga	gcc	tat	gat	ctc	gcg	gcc	ctt	1297
124	Tyr	Asp	Met	Glu	Glu	Lys	Ala	Ala	Arg	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	
125					340				345				350				
127	aag	tac	tgg	gga	cct	tca	acg	cat	ata	aac	ttt	tgc	ata	gag	aat	tac	1345
128	Lys	Tyr	Trp	Gly	Pro	Ser	Thr	His	Ile	Asn	Phe	Ser	Ile	Glu	Asn	Tyr	
129					355				360								
131	caa	gtt	caa	ctt	gag	gaa	atg	aag	aac	atg	agc	aga	cag	gaa	tac	gtt	1393
132	Gln	Val	Gln	Leu	Glu	Glu	Met	Lys	Asn	Met	Ser	Arg	Gln	Glu	Tyr	Val	

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133	370	375	380	
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136	Ala His Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile			
137	385	390	395	400
139	tac aga ggg gtc aca agg cat cac caa cat gga aga tgg caa gcg agg	1489		
140	Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg			
141	405	410	415	
143	ata ggc aga gtt gct ggg aac aaa gac ctt tac ctt ggg acg ttc agc	1537		
144	Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser			
145	420	425	430	
147	acc caa gag gaa gca gca gaa gca tac gat gta gcg gog att aaa ttt	1585		
148	Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala Ile Lys Phe			
149	435	440	445	
151	cgc ggc gca aat gca gtc aca aac ttt gac att tca aga tac gat gtg	1633		
152	Arg Gly Ala Asn Ala Val Thr Asn Phe Asp Ile Ser Arg Tyr Asp Val			
153	450	455	460	
155	gag aga atc atg gcc agt agc aat ctc ctc gct ggg gag ctt gca agg	1681		
156	Glu Arg Ile Met Ala Ser Ser Asn Leu Leu Ala Gly Glu Leu Ala Arg			
157	465	470	475	480
159	cgt aag aaa gat aac gat cct aga aac aag gac ata gac tac aac aag	1729		
160	Arg Lys Lys Asp Asn Asp Pro Arg Asn Lys Asp Ile Asp Tyr Asn Lys			
161	485	490	495	
163	agt gta gta aca agt gtg aac aat gag gaa acg gtt caa gtt caa gca	1777		
164	Ser Val Val Thr Ser Val Asn Asn Glu Glu Thr Val Gln Val Gln Ala			
165	500	505	510	
167	gga aac aac aat aat gaa aac gac tca gag tgg aag atg gtt tta ttt	1825		
168	Gly Asn Asn Asn Asn Glu Asn Asp Ser Glu Trp Lys Met Val Leu Phe			
169	515	520	525	
171	aac cac cct tca cag cag caa cag gca aat ggc aat ggc agt gac caa	1873		
172	Asn His Pro Ser Gln Gln Gln Gln Ala Asn Gly Asn Gly Ser Asp Gln			
173	530	535	540	
175	aaa ata atg aac tgt gga aat tac aga aac agt gca ttt tct atg gcc	1921		
176	Lys Ile Met Asn Cys Gly Asn Tyr Arg Asn Ser Ala Phe Ser Met Ala			
177	545	550	555	560
179	cta caa gat ctt att ggg att gat tcg gtg ggt tct ggg cag cat aat	1969		
180	Leu Gln Asp Leu Ile Gly Ile Asp Ser Val Gly Ser Gly Gln His Asn			
181	565	570	575	
183	agt ctg gac gag tct agc aaa att ggg act cat ttt tca aac acg tca	2017		
184	Met Leu Asp Glu Ser Ser Lys Ile Gly Thr His Phe Ser Asn Thr Ser			
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187	tcg ctg gtg aca agt tta agc agc tca aga gag gct agt cct gag aaa	2065		
188	Ser Leu Val Thr Ser Leu Ser Ser Ser Arg Glu Ala Ser Pro Glu Lys			
189	595	600	605	
191	agg ggt ccc tcg ctt ctg ttc cca atg cct cca atg gaa aca aag att	2113		
192	Arg Gly Pro Ser Leu Leu Phe Pro Met Pro Pro Met Glu Thr Lys Ile			
193	610	615	620	
195	gtg aac ccc att ggt acc agt gtt acc tct tgg cta ccc tca cca acg	2161		
196	Val Asn Pro Ile Gly Thr Ser Val Thr Ser Trp Leu Pro Ser Pro Thr			
197	625	630	635	640

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200 Val Gln Met Arg Pro Ser Pro Ala Ile Ser Leu Ser His Leu Pro Val
201          645          650          655
203 ttt gct tct tgg act gat act taa atggagatag gcacgggtcca tttttcatgt      2263
204 Phe Ala Ser Trp Thr Asp Thr
205          660
207 tatgttatgt aactaaaatt taacttttttc ctctcatcttt tattttetaat ttgatttccct      2323
209 aagttttaaaa aaaaaaaaaa a
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214 <212> TYPE: PRT
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224          20          25          30
227 Ser Ala Ala Thr Val Pro Thr Thr Phe Tyr Met Ser Pro Ser Gln Ser
228          35          40          45
231 His Leu Ser Asn Phe Gly Met Cys Tyr Gly Val Gly Glu Asn Gly Asn
232          50          55          60
235 Phe His Ser Pro Leu Thr Val Met Pro Leu Lys Ser Asp Gly Ser Leu
236 65          70          75          80
239 Cys Ile Leu Glu Ala Leu Lys Arg Ser Gln Thr Gln Val Met Val Pro
240          85          90          95
243 Thr Ser Ser Pro Lys Leu Glu Asp Phe Leu Gly Gly Ala Thr Met Gly
244          100          105          110
247 Thr His Glu Tyr Gly Ser His Glu Arg Gly Leu Ser Leu Asp Ser Ile
248          115          120          125
251 Tyr Tyr Asn Ser Gln Asn Ala Glu Ala Gln Pro Asn Arg Asp Leu Leu
252          130          135          140
255 Ser Gln Pro Phe Arg Gln Gln Gly His Met Ser Val Gln Thr His Pro
256 145          150          155          160
259 Tyr Tyr Ser Gly Leu Ala Cys His Gly Leu Tyr Gln Ala Pro Leu Glu
260          165          170          175
263 Glu Glu Thr Thr Lys Glu Thr His Val Ser Asp Cys Ser Ser Leu Met
264          180          185          190
267 Pro Gln Met Thr Glu Gly Leu Lys Asn Trp Val Ala Pro Thr Arg Glu
268          195          200          205
271 Phe Ser Thr Thr His Gln Gln Val Leu Glu Gln Gln Met Asn Cys Gly Met
272          210          215          220
275 Gly Asn Glu Arg Asn Gly Val Ser Leu Gly Ser Val Gly Cys Gly Glu
276 225          230          235          240
279 Leu Gln Ser Leu Ser Leu Ser Met Ser Pro Gly Ser Gln Ser Ser Cys
280          245          250          255
283 Val Thr Ala Pro Ser Gly Thr Asp Ser Val Ala Val Asp Ala Lys Lys
284          260          265          270
287 Arg Gly His Ala Lys Leu Gly Gln Lys Gln Pro Val His Arg Lys Ser
288          275          280          285

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291 Ile Asp Thr Phe Gly Gln Arg Thr Ser Gln Tyr Arg Gly Val Thr Arg
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295 His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys
296 305      310      315      320
299 Lys Lys Glu Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly
300      325      330      335
303 Tyr Asp Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu
304      340      345      350
307 Lys Tyr Trp Gly Pro Ser Thr His Ile Asn Phe Ser Ile Glu Asn Tyr
308      355      360      365
311 Gln Val Gln Leu Glu Glu Met Lys Asn Met Ser Arg Gln Glu Tyr Val
312      370      375      380
315 Ala His Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile
316 385      390      395      400
319 Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg
320      405      410      415
323 Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser
324      420      425      430
327 Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala Ile Lys Phe
328      435      440      445
331 Arg Gly Ala Asn Ala Val Thr Asn Phe Asp Ile Ser Arg Tyr Asp Val
332      450      455      460
335 Glu Arg Ile Met Ala Ser Ser Asn Leu Leu Ala Gly Glu Leu Ala Arg
336 465      470      475      480
339 Arg Lys Lys Asp Asn Asp Pro Arg Asn Lys Asp Ile Asp Tyr Asn Lys
340      485      490      495
343 Ser Val Val Thr Ser Val Asn Asn Glu Glu Thr Val Gln Val Gln Ala
344      500      505      510
347 Gly Asn Asn Asn Asn Glu Asn Asp Ser Glu Trp Lys Met Val Leu Phe
348      515      520      525
351 Asn His Pro Ser Gln Gln Gln Gln Ala Asn Gly Asn Gly Ser Asp Gln
352      530      535      540
355 Lys Ile Met Asn Cys Gly Asn Tyr Arg Asn Ser Ala Phe Ser Met Ala
356 545      550      555      560
359 Leu Gln Asp Leu Ile Gly Ile Asp Ser Val Gly Ser Gly Gln His Asn
360      565      570      575
363 Met Leu Asp Glu Ser Ser Lys Ile Gly Thr His Phe Ser Asn Thr Ser
364      580      585      590
367 Ser Leu Val Thr Ser Leu Ser Ser Arg Glu Ala Ser Pro Glu Lys
368      595      600      605
371 Arg Gly Pro Ser Leu Leu Phe Pro Met Pro Pro Met Glu Thr Lys Ile
372      610      615      620
375 Val Asn Pro Ile Gly Thr Ser Val Thr Ser Trp Leu Pro Ser Pro Thr
376 625      630      635      640
379 Val Gln Met Arg Pro Ser Pro Ala Ile Ser Leu Ser His Leu Pro Val
380      645      650      655
383 Phe Ala Ser Trp Thr Asp Thr
384      660
387 <210> SEQ ID NO: 3

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2106 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:2180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:2200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:2240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:2266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:2292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:2312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31